

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 4, 2005, 14:01:01 ; Search time 258.605 Seconds  
(without alignments)  
72.265 Million cell updates/sec

Title: US-10-071-512A-2

Perfect score: 92

Sequence: 1 RQIKWFWQRMRKWK 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 6959266 seqs, 1168006243 residues

Total number of hits satisfying chosen parameters: 6959266

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending Patents AA Main:\*

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37: /cgn2\_6/ptodata/1/paa/us41 COMB.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	92	100.0	16	1	PCT-US00-05097-54
2	92	100.0	16	1	PCT-US01-27692A-122
3	92	100.0	16	1	PCT-US01-51600-3
4	92	100.0	16	1	PCT-US02-02837A-2
5	92	100.0	16	1	PCT-US02-05804-29
6	92	100.0	16	1	PCT-US02-05829-29
7	92	100.0	16	1	PCT-US02-11754-3
8	92	100.0	16	1	PCT-US02-13609-21
9	92	100.0	16	1	PCT-US02-20337-1
10	92	100.0	16	1	PCT-US02-22324-14
11	92	100.0	16	1	PCT-US02-27421-2
12	92	100.0	16	1	PCT-US02-27836-55
13	92	100.0	16	1	PCT-US02-30094-5
14	92	100.0	16	1	PCT-US02-33511-113
15	92	100.0	16	1	PCT-US03-01529-10
16	92	100.0	16	1	PCT-US03-01529-14
17	92	100.0	16	1	PCT-US03-02358-71
18	92	100.0	16	1	PCT-US03-02358-75
19	92	100.0	16	1	PCT-US03-02358-75
20	92	100.0	16	1	PCT-US03-02358-75
21	92	100.0	16	1	PCT-US03-02358-75
22	92	100.0	16	1	PCT-US03-02358-75
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44	92	100.0	16	1	PCT-US03-02358-75
45	92	100.0	16	1	PCT-US03-02358-75

ALIGNMENTS

RESULT 1  
PCT-US00-05097-54  
; Sequence 54, Application PC/TUS0005097  
; GENERAL INFORMATION:  
; APPLICANT: Washington University  
; TITLE OF INVENTION: NOVEL TRANSDUCTION MOLECULES AND METHODS  
; TITLE OF INVENTION: FOR USING SAME  
; FILE REFERENCE: 49054-PCT  
; CURRENT APPLICATION NUMBER: PCT/US00/05097  
; CURRENT FILING DATE: 1999-02-28  
; PRIOR APPLICATION NUMBER: 60/122,757  
; PRIOR FILING DATE: 1999-02-28  
; PRIOR APPLICATION NUMBER: 60/151,291  
; PRIOR FILING DATE: 1999-08-29  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 54  
; LENGTH: 16  
; TYPE: PRT

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/ ORGANISM: Unknown
/ FEATURE:
/ OTHER INFORMATION: Synthetic sequence
PCT-US00-05097-54

Query Match      100.0%; Score 92; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 6.2e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWQNRRMKWKK 16
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Db 1 RQIKWQNRRMKWKK 16

RESULT 2
PCT-US01-27692A-122
; Sequence 122, Application PC/TUS0127692A
; GENERAL INFORMATION:
; APPLICANT: Board of Regents, The University of Texas System
; TITLE OF INVENTION: Human and Mouse Targeting Peptides Identified by Phage Display
; FILE REFERENCE: 005774.P003PCT
; CURRENT APPLICATION NUMBER: PCT/US01/27692A
; CURRENT FILING DATE: 2001-09-07
; NUMBER OF SEQ ID NOS: 251
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 122
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
PCT-US01-27692A-122

Query Match      100.0%; Score 92; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 6.2e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWQNRRMKWKK 16
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Db 1 RQIKWQNRRMKWKK 16

RESULT 3
PCT-US01-51600-3
; Sequence 3, Application PC/TUS0151600
; GENERAL INFORMATION:
; APPLICANT: The Board of Trustees of the Leland
; APPLICANT: Stanford Junior University
; TITLE OF INVENTION: pseudo-epsilon RACK Peptide Composition
; TITLE OF INVENTION: and Method for Protection Against Tissue Damage Due to
; TITLE OF INVENTION: Ischemia
; FILE REFERENCE: 58600-8209.W000
; CURRENT APPLICATION NUMBER: PCT/US01/51600
; CURRENT FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: US 60/247,830
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Drosophila antennapedia homeodomain-derived
; OTHER INFORMATION: carrier peptide
PCT-US01-51600-3

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Best Local Similarity 100.0%; Pred. No. 6.2e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 RQIKWQNRRMKWKK 16
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RESULT 4
PCT-US02-02837A-2
; Sequence 2, Application PC/TUS0202837A
; GENERAL INFORMATION:
; APPLICANT: Yale University
; APPLICANT: Rabinovich, Peter
; APPLICANT: Bray-Ward, Patricia
; APPLICANT: Ward, David
; TITLE OF INVENTION: PEPTIDES FOR FACILITATING COMPOSITE RECEPTOR EXPRESSION AND TRANS
; FILE REFERENCE: 044574-5079WO
; CURRENT APPLICATION NUMBER: PCT/US02/02837A
; CURRENT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: 60/265,624
; PRIOR FILING DATE: 2001-02-02
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Drosophila sp.
PCT-US02-02837A-2

Query Match      100.0%; Score 92; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 6.2e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWQNRRMKWKK 16
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Db 1 RQIKWQNRRMKWKK 16

RESULT 5
PCT-US02-05804-29
; Sequence 29, Application PC/TUS0205804
; GENERAL INFORMATION:
; APPLICANT: Rothbard, Jonathan B.
; APPLICANT: Wender, Paul A.
; APPLICANT: McGrane, P. Leo
; APPLICANT: Sista, Lalitha V.S.
; APPLICANT: Kirschberg, Thorsten A.
; APPLICANT: CellGate, Inc.
; TITLE OF INVENTION: Compositions and Methods for Enhancing
; TITLE OF INVENTION: Drug Delivery Across and Into Ocular Tissues
; FILE REFERENCE: 019801-000240PC
; CURRENT APPLICATION NUMBER: PCT/US02/05804
; CURRENT FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: US 09/792,480
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antennapedia homeodomain region residues 43-58
PCT-US02-05804-29

Query Match      100.0%; Score 92; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 6.2e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWQNRRMKWKK 16
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Db 1 RQIKWQNRRMKWKK 16

RESULT 6
PCT-US02-05829-29
; Sequence 29, Application PC/TUS0205829
; GENERAL INFORMATION:
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GenCore version 5.1.6  
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# OM protein - protein search, using sw model

Run on: October 4, 2005, 14:03:57 ; Search time 37.9535 Seconds  
(without alignments)  
73.895 Million cell updates/sec

Title: US-10-071-512A-2

Perfect score: 92

Sequence: 1 RQIKWIFQNRMRKWK 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 800245 seqs, 175286997 residues

Total number of hits satisfying chosen parameters: 800245

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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- 3: /cgn2\_6/ptodata/2/paa/US07\_NEW\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/2/paa/US08\_NEW\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/2/paa/US09\_NEW\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/2/paa/US10\_NEW\_COMB.pep.\*
- 7: /cgn2\_6/ptodata/2/paa/US11\_NEW\_COMB.pep.\*
- 8: /cgn2\_6/ptodata/2/paa/US60\_NEW\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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1	92	100.0	16 1 PCT-US04-35009-7	Sequence 7, Appli
2	92	100.0	16 1 PCT-US05-01251-5	Sequence 5, Appli
3	92	100.0	16 1 PCT-US05-01771-13	Sequence 13, Appli
4	92	100.0	16 1 PCT-US05-05458-9	Sequence 9, Appli
5	92	100.0	16 1 PCT-US04-36200-7	Sequence 7, Appli
6	92	100.0	16 1 PCT-US05-11741-4	Sequence 4, Appli
7	92	100.0	16 1 PCT-US05-16746-1	Sequence 1, Appli
8	92	100.0	16 1 PCT-US05-18985-6	Sequence 6, Appli
9	92	100.0	16 1 PCT-US04-06511A-10	Sequence 10, Appli
10	92	100.0	16 5 US-09-959-873-10	Sequence 10, Appli
11	92	100.0	16 6 US-10-930-313-57	Sequence 57, Appli
12	92	100.0	16 6 US-10-156-570B-21	Sequence 21, Appli
13	92	100.0	16 6 US-10-909-769-6	Sequence 6, Appli
14	92	100.0	16 6 US-10-909-769-8	Sequence 8, Appli
15	92	100.0	16 6 US-10-927-282A-43	Sequence 43, Appli
16	92	100.0	16 6 US-10-700-971C-1	Sequence 1, Appli
17	92	100.0	16 6 US-10-500-671A-10	Sequence 10, Appli
18	92	100.0	16 6 US-10-500-671A-14	Sequence 14, Appli
19	92	100.0	16 6 US-10-878-175B-20	Sequence 20, Appli
20	92	100.0	16 6 US-10-840-060-1	Sequence 1, Appli
21	92	100.0	16 6 US-10-451-314A-12	Sequence 12, Appli
22	92	100.0	16 6 US-10-201-389B-14	Sequence 14, Appli
23	92	100.0	16 6 US-10-991-286A-31	Sequence 31, Appli
24	92	100.0	16 6 US-10-991-286A-49	Sequence 49, Appli
25	92	100.0	16 6 US-10-533-124-4	Sequence 4, Appli

26	92	100.0	16 6 US-10-985-426-1	Sequence 1, Appli
27	92	100.0	16 6 US-10-985-426-19	Sequence 19, Appli
28	92	100.0	16 6 US-10-865-538-21	Sequence 21, Appli
29	92	100.0	16 6 US-10-983-493-6	Sequence 6, Appli
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31	92	100.0	16 6 US-10-899-912A-24	Sequence 24, Appli
32	92	100.0	16 6 US-10-899-912A-42	Sequence 42, Appli
33	92	100.0	16 6 US-10-740-365-29	Sequence 29, Appli
34	92	100.0	16 6 US-10-083-960B-29	Sequence 29, Appli
35	92	100.0	16 6 US-10-462-138A-10	Sequence 10, Appli
36	92	100.0	16 6 US-10-923-112A-20	Sequence 20, Appli
37	92	100.0	16 6 US-10-229-915A-2	Sequence 2, Appli
38	92	100.0	16 6 US-10-287-196A-6	Sequence 6, Appli
39	92	100.0	16 7 US-11-027-967-2	Sequence 2, Appli
40	92	100.0	16 7 US-11-035-714-5	Sequence 5, Appli
41	92	100.0	16 7 US-11-041-103-13	Sequence 13, Appli
42	92	100.0	16 7 US-11-060-005-32	Sequence 32, Appli
43	92	100.0	16 7 US-11-102-432-2	Sequence 2, Appli
44	92	100.0	16 7 US-11-111-463-11	Sequence 11, Appli
45	92	100.0	16 7 US-11-127-903-52	Sequence 52, Appli

## ALIGNMENTS

RESULT 1  
PCT-US04-35009-7  
; Sequence 7, Application PC/TUS0435009  
; GENERAL INFORMATION:  
; APPLICANT: Wake Forest University Health Sciences  
; APPLICANT: Payne, R. Mark  
; TITLE OF INVENTION: NON-VIRAL DELIVERY OF COMPOUNDS TO THE MITOCHONDRIA  
; FILE REFERENCE: 9151-37WO  
; CURRENT APPLICATION NUMBER: PCT/US04/35009  
; CURRENT FILING DATE: 2004-10-22  
; PRIOR APPLICATION NUMBER: US 60/514,892  
; PRIOR FILING DATE: 2003-10-24  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 7  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Drosophila melanogaster  
PCT-US04-35009-7

Query Match 100.0%; Score 92; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 6.7e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RQIKWIFQNRMRKWK 16  
Db 1 RQIKWIFQNRMRKWK 16

RESULT 2  
PCT-US05-01251-5  
; Sequence 5, Application PC/TUS0501251  
; GENERAL INFORMATION:  
; APPLICANT: LAUDANNA, CARLO  
; APPLICANT: BUTCHER, EUGENE C.  
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF RHOA SIGNALING  
; FILE REFERENCE: STAN-346WO  
; CURRENT APPLICATION NUMBER: PCT/US05/01251  
; CURRENT FILING DATE: 2005-01-25  
; PRIOR APPLICATION NUMBER: 60/537,142  
; PRIOR FILING DATE: 2004-01-16  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: H. sapien  
PCT-US05-01251-5

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Query Match      100.0%; Score 92; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 6.7e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWQNRRMKWKK 16
DB 1 RQIKWQNRRMKWKK 16

RESULT 3
PCT-US05-01771-13
; Sequence 13, Application PC/TUS0501771
; GENERAL INFORMATION:
; APPLICANT: Georgia Tech Research Corporation
; APPLICANT: Bao, Gang
; APPLICANT: Nitin, Nitin
; TITLE OF INVENTION: Activatable Probes and Methods For In Vivo Gene Detection
; FILE REFERENCE: 820701-2820
; CURRENT APPLICATION NUMBER: PCT/US05/01771
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: 10/179,730
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: 60/300,672
; PRIOR FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: 60/303,258
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 60/538,381
; PRIOR FILING DATE: 2004-01-21
; PRIOR APPLICATION NUMBER: 60/538,382
; PRIOR FILING DATE: 2004-01-21
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 13
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Protein Transduction Domain
PCT-US05-01771-13

Query Match      100.0%; Score 92; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 6.7e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWQNRRMKWKK 16
DB 1 RQIKWQNRRMKWKK 16

RESULT 4
PCT-US05-05458-9
; Sequence 9, Application PC/TUS0505458
; GENERAL INFORMATION:
; APPLICANT: Dana-Farber Cancer Institute, Inc., et al.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
; TITLE OF INVENTION: TREATMENT AND PREVENTION OF HIV INFECTION USING TRIMSALPHA
; FILE REFERENCE: DFN-058PC
; CURRENT APPLICATION NUMBER: PCT/US05/05458
; CURRENT FILING DATE: 2005-03-02
; PRIOR APPLICATION NUMBER: 60/548,139
; PRIOR FILING DATE: 2004-02-25
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Drosophila
PCT-US05-05458-9

Query Match      100.0%; Score 92; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 6.7e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 5
PCT-US04-36200-7
; Sequence 7, Application PC/TUS0436200
; GENERAL INFORMATION:
; APPLICANT: THE CBR INSTITUTE FOR BIOMEDICAL RESEARCH, INC.
; APPLICANT: LIEBERMAN, JUDY
; APPLICANT: HAMAR, PETER
; TITLE OF INVENTION: METHODS FOR TREATING AND PREVENTING ISCHEMIA-REPERFUSION
; TITLE OF INVENTION: INJURY USING RNA INTERFERING AGENTS
; FILE REFERENCE: 03393-55221
; CURRENT APPLICATION NUMBER: PCT/US04/36200
; CURRENT FILING DATE: 2004-11-01
; PRIOR APPLICATION NUMBER: 60/516,172
; PRIOR FILING DATE: 2003-10-30
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patentin Ver. 3.2
; SEQ ID NO 7
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Drosophila sp.
PCT-US04-36200-7

Query Match      100.0%; Score 92; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 6.7e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWQNRRMKWKK 16
DB 1 RQIKWQNRRMKWKK 16

RESULT 6
PCT-US05-11741-4
; Sequence 4, Application PC/TUS0511741
; GENERAL INFORMATION:
; APPLICANT: Regents of the University of California
; APPLICANT: Pandol, Stephen J
; APPLICANT: Gukovskaya, Anna
; APPLICANT: Yazbeck, Moussa
; APPLICANT: Eibl, Guido
; APPLICANT: Boros, Laszlo G
; APPLICANT: Sato, Akihiko
; TITLE OF INVENTION: COMPOSITIONS COMPRISING PLANT-DERIVED POLYPHENOLIC COMPOUNDS AND
; TITLE OF INVENTION: INHIBITORS OF REACTIVE OXYGEN SPECIES AND METHODS OF USING
; FILE REFERENCE: 034044.021.1
; CURRENT APPLICATION NUMBER: PCT/US05/11741
; CURRENT FILING DATE: 2005-04-13
; PRIOR APPLICATION NUMBER: US 10/260,609
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 60/562,315
; PRIOR FILING DATE: 2004-04-15
; PRIOR APPLICATION NUMBER: US 10/824,597
; PRIOR FILING DATE: 2004-04-15
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 4
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
PCT-US05-11741-4

Query Match      100.0%; Score 92; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 6.7e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWQNRRMKWKK 16
```

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OM protein - protein search, using sw model

Run on: October 4, 2005, 14:20:28 ; Search time 18.6047 Seconds  
(without alignments)  
82.746 Million cell updates/sec

Title: US-10-071-512A-2

Perfect score: 92

Sequence: 1 RQIKIWQNRRMKWKK 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	92	100.0	33	2 S57235	antennapedia prote
2	92	100.0	42	2 I65241	homeotic protein H
3	92	100.0	45	2 PC1216	homeotic protein D
4	92	100.0	48	2 IS1439	homeobox protein -
5	92	100.0	66	2 S15538	homeotic protein H
6	92	100.0	66	2 S15536	homeotic protein H
7	92	100.0	71	2 JC1161	homeotic protein 3
8	92	100.0	71	2 A60084	homeotic protein H
9	92	100.0	74	2 D34510	homeotic protein H
10	92	100.0	75	2 S58852	homeotic protein S
11	92	100.0	75	2 IS1341	homeo box protein
12	92	100.0	76	2 C43559	homeotic protein R
13	92	100.0	78	2 IS1342	homeo box protein
14	92	100.0	81	2 B29585	homeotic protein H
15	92	100.0	81	2 S47605	homeotic protein H
16	92	100.0	82	2 S08302	homeotic protein H
17	92	100.0	83	2 S50066	homeotic protein H
18	92	100.0	83	2 S47603	homeotic protein H
19	92	100.0	86	2 A34510	homeotic protein H
20	92	100.0	86	2 S08303	homeotic protein H
21	92	100.0	86	2 JT0489	homeotic protein Z
22	92	100.0	87	2 S05889	homeotic protein H
23	92	100.0	88	2 A03317	homeotic protein M
24	92	100.0	96	2 S08639	homeotic protein z
25	92	100.0	96	2 A05266	homeotic protein H
26	92	100.0	97	2 C27176	homeotic protein H
27	92	100.0	97	2 A24779	homeotic protein m
28	92	100.0	103	2 A32167	homeotic protein H
29	92	100.0	105	2 S47602	homeotic protein H

30	92	100.0	105	2 A27471	homeotic protein R
31	92	100.0	106	2 S36448	homeotic protein s
32	92	100.0	107	2 B61045	homeotic protein T
33	92	100.0	113	2 T10775	homeobox protein -
34	92	100.0	118	2 A24777	homeotic protein H
35	92	100.0	118	2 JT0273	homeotic protein H
36	92	100.0	119	2 B24777	homeotic protein M
37	92	100.0	119	2 A03314	homeotic protein m
38	92	100.0	138	2 S20087	homeotic protein b
39	92	100.0	148	2 PC4071	homeobox A5 protei
40	92	100.0	153	1 WJHU3C	homeotic protein H
41	92	100.0	153	1 WJMSX6	homeotic protein H
42	92	100.0	158	2 A27348	homeotic protein H
43	92	100.0	209	2 A43553	homeotic protein H
44	92	100.0	217	1 WJHU2C	homeotic protein H
45	92	100.0	217	1 WJMSX2	homeotic protein H

ALIGNMENTS

RESULT 1

S57235  
antennapedia protein (clone pl105) - fruit fly (Drosophila pseudoobscura) (fragment)  
C:Species: Drosophila pseudoobscura  
C>Date: 10-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 16-Aug-2004  
C:Accession: S57235  
R:Randazzo, F.M.; Seeger, M.A.; Huss, C.A.; Sweeney, M.A.; Cecil, J.K.; Kaufman, T.C.  
Genetics 133, 319-330, 1993  
A>Title: Structural changes in the antennapedia complex of Drosophila pseudoobscura.  
A:Reference number: S57224  
A:Accession: S57235  
A:Molecule type: DNA  
A:Residues: 1-33 <RAN>  
A:Cross-references: EMBL:X77711  
C:Genetics:  
A:Gene: FlyBase:Antp  
A:Cross-references: FlyBase:FBgn0012693  
C:Superfamily: homeobox homology  
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation  
F:1-22/Domain: homeobox homology (fragment) <HOX>

Query Match 100.0%; Score 92; DB 2; Length 33;  
Best Local Similarity 100.0%; Pred. No. 1.6e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKIWQNRRMKWKK 16

DB 7 RQIKIWQNRRMKWKK 22

RESULT 2

I65241  
homeotic protein Hox-A - rat (fragment)  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 27-Feb-1997 #sequence\_revision 27-Feb-1997 #text\_change 16-Aug-2004  
C:Accession: I65241  
R:Sakoyama, Y.; Mizuta, I.; Ogasawara, N.; Yoshikawa, H.  
Biochem. Genet. 32, 351-360, 1994  
A>Title: Cloning of rat homeobox genes.  
A:Reference number: I52340; MUID:95217128; PMID:7702549  
A:Accession: I65241  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-42 <RES>  
A:Cross-references: GB:S76290; NID:g913077  
C:Genetics:  
A:Gene: Hox-A; Hox-1  
C:Superfamily: homeobox homology  
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation  
F:1-40/Domain: homeobox homology (fragment) <HOX>

Query Match 100.0%; Score 92; DB 2; Length 42;



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QM protein - protein search, using sw model

Run on: October 4, 2005, 14:08:33 ; Search time 86.3256 Seconds  
(without alignments)  
94.911 Million cell updates/sec

Title: US-10-071-512A-2

Perfect score: 92

Sequence: 1 RQIKWQNRRMKWKK 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot\_03:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	92	100.0	33	Q86FU0	Q86fu0 drosophila
2	92	100.0	39	O57368	O57368 brachydanio
3	92	100.0	42	Q80WH6	Q80wh6 rattus sp.
4	92	100.0	43	O57359	O57359 brachydanio
5	92	100.0	44	Q6L8T3	Q6l8t3 lampetra la
6	92	100.0	46	Q9PVR9	Q9pvr9 oryzias lat
7	92	100.0	47	Q6IT83	Q6it83 oncopeltus
8	92	100.0	48	1 HXB6 XENLA	P31256 xenopus lae
9	92	100.0	49	1 HXA5 SHEEP	Q28599 ovis aries
10	92	100.0	51	Q23743	Q23743 ctenodrilus
11	92	100.0	51	Q26407	Q26407 ctenodrilus
12	92	100.0	51	Q27413	Q27413 ctenodrilus
13	92	100.0	51	Q7JPR7	Q7jpr7 ctenodrilus
14	92	100.0	57	Q9PVR8	Q9pvr8 oryzias lat
15	92	100.0	58	Q25208	Q25208 junonia coe
16	92	100.0	58	Q9Y188	Q9y188 priapulus c
17	92	100.0	58	O57362	O57362 brachydanio
18	92	100.0	59	Q8WRM9	Q8wrn9 lithobius a
19	92	100.0	59	Q9NB42	Q9nb42 anopheles g
20	92	100.0	59	Q9PVR5	Q9pvr5 oryzias lat
21	92	100.0	60	Q77139	Q77139 archegozete
22	92	100.0	60	Q77143	Q77143 archegozete
23	92	100.0	60	Q80WH4	Q80wh4 rattus sp.
24	92	100.0	60	Q80WH7	Q80wh7 rattus sp.
25	92	100.0	60	Q8QGL2	Q8qgl2 petromyzon
26	92	100.0	60	Q8QGL3	Q8qgl3 petromyzon
27	92	100.0	60	Q8QGL5	Q8qgl5 petromyzon
28	92	100.0	60	Q8QGL6	Q8qgl6 petromyzon
29	92	100.0	60	Q8QGL7	Q8qgl7 petromyzon
30	92	100.0	60	Q8QGL8	Q8qgl8 petromyzon
31	92	100.0	61	Q27910	Q27910 polyandroca

32 92 100.0 63 2 O77138 archegozete  
33 92 100.0 63 2 Q8MXB2 holopneuste  
34 92 100.0 66 2 O57356 brachydanio  
35 92 100.0 69 2 Q9BMF7 haliotis ae  
36 92 100.0 69 2 Q9U9T4 nereis vire  
37 92 100.0 70 2 Q967W5 folsomia ca  
38 92 100.0 70 2 Q801B4 latimeria m  
39 92 100.0 71 1 HXA7 SHEEP  
40 92 100.0 71 1 HXC5 NOTVI  
41 92 100.0 71 2 Q6EBC8 bugula turr  
42 92 100.0 71 2 Q9PVS1 oryzias lat  
43 92 100.0 71 2 Q9PVS3 oryzias lat  
44 92 100.0 73 2 Q86D93 spadella ce  
45 92 100.0 73 2 Q9Y186 priapulus c

#### ALIGNMENTS

RESULT 1

Q86FU0 PRELIMINARY; PRT; 33 AA.  
AC Q86FU0;  
DT 01-JUN-2003 (Tremblrel. 24, Created)  
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)  
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)  
DE Antennapedia complex (Fragment).  
GN Name=ANT-C;  
OS Drosophila pseudoobscura (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7237;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93292933; PubMed=80999892;  
RA Randazzo F.M., Seeger M.A., Huss C.A., Sweeney M.A., Cecil J.K.,  
RA Kaufman T.C.;  
RT "Structural changes in the antennapedia complex of Drosophila  
RT pseudoobscura";  
RL Genetics 134:319-330(1993).  
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).  
DR EMBL; S63455; AAP13946.1; -.  
DR HSSP; P02833; 1HOM.  
DR GO; GO:0005634; C:nucleus; IEA.  
DR GO; GO:0003700; P:transcription factor activity; IEA.  
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
DR InterPro; IPR001356; Homeobox.  
DR InterPro; IPR009057; Homeodomain\_like.  
DR PRINTS; P00024; HOMEBOX.  
DR Probom; PD00010; Homeobox; 1.  
DR PROSITE; PS50071; HOMEBOX\_2; 1.  
KW DNA-binding; Homeobox; Nuclear protein.  
FT NON\_TER 1  
FT NON\_TER 33  
SQ SEQUENCE 33 AA; 3963 MW; D78E37ED81PD45DF CRC64;

Query Match 100.0%; Score 92; DB 2; Length 33;

Best Local Similarity 100.0%; Pred. No. 3.1e-07;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWQNRRMKWKK 16

|||||

Db 7 RQIKWQNRRMKWKK 22

RESULT 2

O57368 PRELIMINARY; PRT; 39 AA.  
ID O57368;  
AC O57368;

DT 01-JUN-1998 (Tremblrel. 06, Created)

DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)

DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)

DE HoxC5 protein (Fragment).  
 GN Name=hoxc5a; Synonyms=hoxc5;  
 OS Brachydanio rerio (Zebrafish) (Danio rerio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 OX NCBI\_TaxID=7955;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Prince V.E., Joly L., Ekker M., Ho R.K.;  
 RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.  
 CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).  
 DR EMBL; Y14539; CAA74874.1; -.  
 DR HSP; P02833; IHOM.  
 DR ZFIN; ZDB-GENE-980526-533; hoxc5a.  
 DR GO; GO:0005634; C:nucleus; IEA.  
 DR GO; GO:0003700; F:transcription factor activity; IEA.  
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro; IPR001356; Homeobox.  
 DR InterPro; IPR009057; Homeodomain\_like.  
 DR Pfam; PF00046; Homeobox; 1.  
 DR PRINTS; PR00024; HOMEBOX.  
 DR PRINTS; PR00031; HTHREPRESSR.  
 DR ProDom; PD000010; Homeobox; 1.  
 DR SMART; SM00389; HOX; 1.  
 DR PROSITE; PS00027; HOMEBOX\_1; 1.  
 DR PROSITE; PS00071; HOMEBOX\_2; 1.  
 KW DNA-binding; Homeobox; Nuclear protein.  
 FT NON\_TER 1  
 SQ SEQUENCE 39 AA; 4827 MW; 592A0FEC12E58860 CRC64;

Query Match 100.0%; Score 92; DB 2; Length 39;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-07;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWIFQNRKWK 16  
 |||||  
 Db 14 RQIKWIFQNRKWK 29

RESULT 3  
 Q80WH6 PRELIMINARY; PRT; 42 AA.  
 ID Q80WH6;  
 AC Q80WH6;  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Hox-A|Hox-1 (Fragment).  
 GN Name=Hox-A|Hox-1;  
 OS Rattus sp.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10118;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=95217128; PubMed=7702549;  
 RA Sakoyama Y., Mizuta I., Ogasawara N., Yoshikawa H.;  
 RT "Cloning of rat homeobox genes."  
 RL Biochem. Genet. 32:351-360(1994).  
 CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).  
 DR EMBL; S76290; AAP31864.1; -.  
 DR HSP; P02833; IHOM.  
 DR GO; GO:0005634; C:nucleus; IEA.  
 DR GO; GO:0003700; F:transcription factor activity; IEA.  
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro; IPR001356; Homeobox.  
 DR InterPro; IPR009057; Homeodomain\_like.  
 DR Pfam; PF00046; Homeobox; 1.  
 DR PRINTS; PR00024; HOMEBOX.  
 DR PRINTS; PR00031; HTHREPRESSR.  
 DR ProDom; PD000010; Homeobox; 1.

DR SMART; SM00389; HOX; 1.  
 DR PROSITE; PS00027; HOMEBOX\_1; 1.  
 DR PROSITE; PS00071; HOMEBOX\_2; 1.  
 KW DNA-binding; Homeobox; Nuclear protein.  
 FT NON\_TER 1  
 FT NON\_TER 42  
 SQ SEQUENCE 42 AA; 5494 MW; 38E5153B92216FE9 CRC64;

Query Match 100.0%; Score 92; DB 2; Length 42;  
 Best Local Similarity 100.0%; Pred. No. 4e-07;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWIFQNRKWK 16  
 |||||  
 Db 25 RQIKWIFQNRKWK 40

RESULT 4  
 O57359 PRELIMINARY; PRT; 43 AA.  
 ID O57359;  
 AC O57359;  
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)  
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Hoxa5 protein (Fragment).  
 GN Name=hoxb5b; Synonyms=hoxa5;  
 OS Brachydanio rerio (Zebrafish) (Danio rerio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 OX NCBI\_TaxID=7955;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Prince V.E., Joly L., Ekker M., Ho R.K.;  
 RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.  
 CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).  
 DR EMBL; Y14526; CAA74861.1; -.  
 DR HSP; P02833; IHOM.  
 DR ZFIN; ZDB-GENE-000823-6; hoxb5b.  
 DR GO; GO:0005634; C:nucleus; IEA.  
 DR GO; GO:0003700; F:transcription factor activity; IEA.  
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro; IPR001356; Homeobox.  
 DR InterPro; IPR009057; Homeodomain\_like.  
 DR Pfam; PF00046; Homeobox; 1.  
 DR PRINTS; PR00024; HOMEBOX.  
 DR ProDom; PD000010; Homeobox; 1.  
 DR PROSITE; PS00027; HOMEBOX\_1; 1.  
 DR PROSITE; PS00071; HOMEBOX\_2; 1.  
 KW DNA-binding; Homeobox; Nuclear protein.  
 FT NON\_TER 1  
 SQ SEQUENCE 43 AA; 5050 MW; 53034C37F3DFA596 CRC64;

Query Match 100.0%; Score 92; DB 2; Length 43;  
 Best Local Similarity 100.0%; Pred. No. 4.1e-07;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWIFQNRKWK 16  
 |||||  
 Db 10 RQIKWIFQNRKWK 25

RESULT 5  
 Q6L8J3 PRELIMINARY; PRT; 44 AA.  
 ID Q6L8J3;  
 AC Q6L8J3;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE LjHox7m Homeobox (Fragment).  
 GN Name=LjHox7m;  
 OS Lampetra japonica (Japanese lamprey) (Entosphenus japonicus).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 4, 2005, 14:07:33 ; Search time 89.6744 Seconds  
(without alignments)  
69.007 Million cell updates/sec

Title: US-10-071-512A-2  
Perfect score: 92  
Sequence: 1 RQIKWFWQRMRKWK 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

- 1: Geneseqp1980s:\*
- 2: Geneseqp1990s:\*
- 3: Geneseqp2000s:\*
- 4: Geneseqp2001s:\*
- 5: Geneseqp2002s:\*
- 6: Geneseqp2003as:\*
- 7: Geneseqp2003bs:\*
- 8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	92	100.0	16	2 AAW45974	Aaw45974 Cysteine
2	92	100.0	16	2 AAW33407	Aaw33407 Peptide 4
3	92	100.0	16	2 AAW33410	Aaw33410 D-form pe
4	92	100.0	16	2 AAW82958	Aaw82958 Oestrogen
5	92	100.0	16	2 AAW56397	Aaw56397 Preferred
6	92	100.0	16	2 AAW71270	Aaw71270 Antennape
7	92	100.0	16	2 AAW71316	Aaw71316 Antennape
8	92	100.0	16	2 AAW30508	Aaw30508 Drosophil
9	92	100.0	16	2 AAW91046	Aaw91046 Internali
10	92	100.0	16	2 AAW52102	Aaw52102 Peptide f
11	92	100.0	16	2 AAY00859	Aay00859 Peptide p
12	92	100.0	16	2 AAY13509	Aay13509 Signal ee
13	92	100.0	16	3 AAY87920	Aay87920 Drosophil
14	92	100.0	16	3 AAW27060	Aaw27060 Beta-cate
15	92	100.0	16	3 AAY93667	Aay93667 Peptide w
16	92	100.0	16	3 AAY67966	Aay67966 Carboxyfl
17	92	100.0	16	3 AAY93551	Aay93551 Amino aci
18	92	100.0	16	3 AAY55818	Aay55818 Signal ee
19	92	100.0	16	3 AAY71008	Aay71008 Drosophil
20	92	100.0	16	3 AAY51212	Aay51212 Antennape
21	92	100.0	16	3 AAY51167	Aay51167 Drosophil
22	92	100.0	16	3 AAB10343	Aab10343 Peptide A
23	92	100.0	16	3 AAB19251	Aab19251 Fragment
24	92	100.0	16	3 AAY93178	Aay93178 Protegrin
25	92	100.0	16	3 AAB35694	Aab35694 Peptide a

26	92	100.0	16	3 AAB22025	Aab22025 Membrane
27	92	100.0	16	3 AAB29423	Aab29423 ANTP pept
28	92	100.0	16	3 AAB03927	Aab03927 Internali
29	92	100.0	16	3 AAY93954	Aay93954 Peptide u
30	92	100.0	16	3 AAB29574	Aab29574 Antennape
31	92	100.0	16	3 ADE14785	Ade14785 Carrier m
32	92	100.0	16	3 ADE14761	Ade14761 Drosophil
33	92	100.0	16	4 AAB73091	Aab73091 Rheumatol
34	92	100.0	16	4 AAB60004	Aab60004 Internali
35	92	100.0	16	4 AAB70753	Aab70753 Cell memb
36	92	100.0	16	4 AAE02974	Aae02974 Protein t
37	92	100.0	16	4 AAB60671	Aab60671 Antennape
38	92	100.0	16	4 AAU06064	Aau06064 Drosophil
39	92	100.0	16	4 AAB49914	Aab49914 Hif-lalph
40	92	100.0	16	4 AAB66996	Aab66996 Antennape
41	92	100.0	16	4 AAU00813	Aau00813 Fruit fly
42	92	100.0	16	4 AAE12205	Aae12205 Membrane
43	92	100.0	16	5 ABB78030	Abb78030 Peptide d
44	92	100.0	16	5 ABB78985	Abb78985 Cell pene
45	92	100.0	16	5 ABB78214	Abb78214 Amino aci

## ALIGNMENTS

RESULT 1  
AAW45974  
ID AAW45974 standard; peptide; 16 AA.  
XX  
AC AAW45974;  
XX  
DT 01-JUL-1998 (first entry)  
XX  
DE Cysteine protease inhibiting peptide for preventing cell death.  
XX  
KW Neuronal cell death; neurodegenerative disorder; inhibition;  
KW Cysteine protease; cardiovascular; liver disease.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 1 /note= "N-3-nitro-2-pyridyl-sulphenyl-Arg"  
XX  
PN WO9735876-A1.  
XX  
PD 02-OCT-1997.  
XX  
PF 04-MAR-1997; 97WO-US004158.  
XX  
PR 04-MAR-1996; 96US-00610220.  
XX  
PA (UYCO ) UNIV COLUMBIA NEW YORK.  
XX  
PI Troy CM;  
XX  
WPI; 1997-489561/45.  
XX  
PT New cysteine protease inhibiting peptide(s) for preventing cell death -  
PT in cases of neurodegenerative, cardiovascular and liver diseases, and  
PT their peptidomimetics, and general method for identifying enzyme  
PT inhibiting peptides.  
XX  
PS Claim 8; Page 68; 112pp; English.  
XX

CC This sequence represents a specifically claimed peptide of the formula: V  
CC -(AA1)n-Cys(V')-(AA2)m-V' (I), in which n and m = 0-5, totalling 2-5; if  
CC n =1, AA1 = Ala; if n = 2, (AA1)n = Gln-Ala; and if n =3 or more, (AA1)n  
CC = (X)p-Gln-Ala; X = any amino acid; p = 1-3, depending on value of n; if  
CC m = 1, AA2 = Arg; if m =2, (AA2)n = Arg-Gly; if m = 3 or more, (AA2)n =  
CC Arg-Gly-(X)q; q = 1-3, depending on value of m; V, V' and V'', any or all  
CC of which may be absent, = agent able to direct the compound to a specific  
CC cell. The peptides are inhibitors of cysteine proteases, specifically

CC interleukin-1 beta converting enzyme (ICE). They inhibit death of cells,  
 CC particularly in humans, and can be used to treat neurodegenerative  
 CC diseases (e.g. ageing, Alzheimer's, Machado-Joseph, Parkinson's or  
 CC Huntington's diseases, multiple sclerosis, muscular dystrophy, stroke),  
 CC cardiovascular disease and liver disorders. The peptides should be more  
 CC specific than pseudosubstrate inhibitors  
 XX  
 SQ Sequence 16 AA;

Query Match 100.0%; Score 92; DB 2; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-06;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKIWFQNRMRMKWK 16  
 |||||  
 DB 1 RQIKIWFQNRMRMKWK 16

RESULT 2  
 AAW33407  
 ID AAW33407 standard; peptide; 16 AA.  
 XX  
 AC AAW33407;

XX 27-AUG-2003 (revised)  
 DT 17-MAR-1998 (first entry)  
 XX  
 DE Peptide 43-58 of homeodomain Antp.  
 XX homeodomain; transcription factor; Antennapedia; Antp; vector;  
 KW transfection; hydrophobic.  
 KW  
 OS Unidentified.  
 XX

PN WO9712912-A1.  
 PD 10-APR-1997.  
 XX  
 PF 04-OCT-1996; 96WO-FR001553.  
 XX  
 PR 05-OCT-1995; 95FR-00011714.  
 XX (CNRS ) CNRS CENT NAT RECH SCI.  
 PA Chassaing G, Prochiantz A;  
 PI  
 XX WPI; 1997-226166/20.

XX New peptide(s) of high hydrophobic amino acid content - useful as vectors  
 PT for delivering peptides and nucleic acids to cells.  
 XX  
 PS Claim 1; Page 7; 35pp; French.

XX New peptides are provided which are 16 amino acids long and which are  
 CC analogues of the peptide corresponding to residues 43-58 of the  
 CC Antennapedia transcription factor homeodomain (AntpHD). The peptides  
 CC contain 6-10 hydrophobic amino acids. They have the general formula: X1-  
 CC X2-X3-X4-X5-Trp-X8-X9-X10-X11-X12-X13-X14-X15-X16 or X16-X15-X14-X13-  
 CC X12-X11-X10-X9-X8-X7-Trp-X5-X4-X3-X2-X1 in which X1-X5 and X7-X16 are any  
 CC alpha-amino acids, provided that: (1) the peptide contains 6-10  
 CC hydrophobic amino acids; (2) X3 and X5 are not both Val; and (3) the  
 CC natural Antp 43-58 sequence RQIKIWFQNRMRMKWK (i.e. the present sequence)  
 CC is excluded. Specific examples of these peptides are given in AAW33408 -  
 CC AAW33416. The peptides are used as vectors for introducing into live  
 CC cells compounds which affect cell function, esp. peptides and nucleic  
 CC acids. They can cross cellular membranes and reach various cell  
 CC compartments. They are as effective as helix 3 of a homeodomain peptide.  
 CC (Updated on 27-AUG-2003 to correct OS field.)

XX Sequence 16 AA;  
 Query Match 100.0%; Score 92; DB 2; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-06;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RQIKIWFQNRMRMKWK 16  
 |||||  
 DB 1 RQIKIWFQNRMRMKWK 16

RESULT 3  
 AAW33410  
 ID AAW33410 standard; peptide; 16 AA.  
 XX  
 AC AAW33410;

XX 17-MAR-1998 (first entry)  
 DT  
 XX D-form peptide 43-58 of homeodomain Antp.  
 DE homeodomain; transcription factor; Antennapedia; Antp; vector;  
 KW transfection; hydrophobic.  
 KW  
 OS Synthetic.  
 XX

XX Key Location/Qualifiers  
 FH Misc-difference 1..16  
 FT /note= "all residues are D-form"  
 FT Modified-site 1  
 FT /note= "in determining the ability of this sequence to be  
 FT internalised in cells, a biotin-aminopentanoyl group was  
 FT attached to the N-terminal"

XX WO9712912-A1.  
 XX  
 PD 10-APR-1997.  
 XX  
 PF 04-OCT-1996; 96WO-FR001553.  
 XX  
 PR 05-OCT-1995; 95FR-00011714.  
 XX (CNRS ) CNRS CENT NAT RECH SCI.  
 PA Chassaing G, Prochiantz A;  
 PI  
 XX WPI; 1997-226166/20.

XX New peptide(s) of high hydrophobic amino acid content - useful as vectors  
 PT for delivering peptides and nucleic acids to cells.  
 XX  
 PS Disclosure; Page 7; 35pp; French.

XX New peptides are provided which are 16 amino acids long and which are  
 CC analogues of the peptide corresponding to residues 43-58 of the  
 CC Antennapedia transcription factor homeodomain (AntpHD). The peptides  
 CC contain 6-10 hydrophobic amino acids. They have the general formula: X1-  
 CC X2-X3-X4-X5-Trp-X8-X9-X10-X11-X12-X13-X14-X15-X16 or X16-X15-X14-X13-  
 CC X12-X11-X10-X9-X8-X7-Trp-X5-X4-X3-X2-X1 in which X1-X5 and X7-X16 are any  
 CC alpha-amino acids, provided that: (1) the peptide contains 6-10  
 CC hydrophobic amino acids; (2) X3 and X5 are not both Val; and (3) the  
 CC natural Antp 43-58 sequence RQIKIWFQNRMRMKWK (see AAW33407) is excluded.  
 CC The present sequence (the D-form of the 43-58 peptide) is a specific  
 CC example of the new peptides. The peptides are used as vectors for  
 CC introducing into live cells compounds which affect cell function,  
 CC especially peptides and nucleic acids. They can cross cellular membranes  
 CC and reach various cell compartments. They are as effective as helix 3 of  
 CC a homeodomain peptide

XX Sequence 16 AA;

Query Match 100.0%; Score 92; DB 2; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-06;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKIWFQNRMRMKWK 16  
 |||||

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 4, 2005, 14:07:33 ; Search time 151.326 Seconds  
(without alignments)  
69.007 Million cell updates/sec

Title: US-10-071-512A-3

Perfect score: 133  
Sequence: 1 GWTLSAGYLLGKINKLALAKKIL 27

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

- 1: Geneseqp1980s:\*
- 2: Geneseqp1990s:\*
- 3: Geneseqp2000s:\*
- 4: Geneseqp2001s:\*
- 5: Geneseqp2002s:\*
- 6: Geneseqp2003as:\*
- 7: Geneseqp2003bs:\*
- 8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	133	100.0	27	2	Aay00858 Peptide #
2	133	100.0	27	3	Aab17999 Membrane
3	133	100.0	27	3	Aab22024 Membrane
4	133	100.0	27	3	Aab29575 Transport
5	133	100.0	27	4	Aae02978 Hydrophob
6	133	100.0	27	4	Aae06072 Transport
7	133	100.0	27	4	Aae12488 Membrane
8	133	100.0	27	5	Abb78215 Amino aci
9	133	100.0	27	5	Abb73370 Exemplary
10	133	100.0	27	5	Aae22207 Transport
11	133	100.0	27	6	Abp72305 Transport
12	133	100.0	27	6	Aae35392 Transport
13	133	100.0	27	6	Abp43124 Human mem
14	133	100.0	27	6	Abb282915 Transport
15	133	100.0	27	7	Adg28015 Synthetic
16	133	100.0	27	7	Adj73523 Exemplary
17	133	100.0	27	7	Adl88651 Transport
18	133	100.0	27	7	Adl23664 Galanin (
19	133	100.0	27	8	Adh89687 Cell pene
20	133	100.0	27	8	Adj53157 CH1 delet
21	133	100.0	27	8	Adj52118 CH1 delet
22	133	100.0	27	8	Adj78885 Transport
23	133	100.0	27	8	Adk15590 Membrane
24	133	100.0	27	8	Ado26479 Galanin a
25	133	100.0	27	8	

#### ALIGNMENTS

RESULT 1

AA00858

ID AAY00858 standard; peptide; 27 AA.

XX AC AAY00858;

XX DT 20-MAY-1999 (first entry)

XX DE Peptide #3 used in membrane-permeable construct.

XX KW Membrane-permeable construct; lipid membrane; membrane transport;  
XX KW oligonucleotide delivery; cancer therapy; signal transduction; inhibitor;  
XX KW gene therapy; transcription; translation; expression; replication.

XX OS Synthetic.

XX PN WO9905302-Al.

XX PD 04-FEB-1999.

XX PF 16-JUL-1998; 98WO-US014761.

XX PR 24-JUL-1997; 97US-0053678P.

XX (PEKE ) PERKIN-ELMER CORP.

XX Langel U, Bartfai T, Pooga M, Valkna A, Saar K, Hallbrink M;

XX WPI; 1999-142952/12.

XX New membrane-permeable constructs - comprise a peptide linked by a labile bond to a nucleic acid analogue capable of hybridising with an intracellular polynucleotide.

XX Claim 5; Page 41; 60pp; English.

XX This sequence represents a peptide used in the construct of the invention. The construct is a membrane-permeable construct for transport across a lipid membrane, which comprises: (a) a nucleic acid analogue capable of hybridising with an intracellular polynucleotide (PN); (b) a peptide; and (c) a labile bond linking the nucleic acid analogue and the peptide. The membrane-permeable constructs can be used for delivery of oligonucleotides, nucleic acids and nucleic acid analogues into cells. They can be used for e.g. cancer therapy, signal transduction studies, identifying new intracellular drug targets or gene therapy. They can also be used for selectively inhibiting DNA transcription, RNA translation, RNA or DNA expression, DNA replication, or an DNA or RNA regulatory function of preselected DNA or RNA sequences in a living cell

26	133	100.0	27	8	ADM97018
27	133	100.0	27	8	ADO43344
28	133	100.0	27	8	ADO80842 Synthetic
29	133	100.0	27	8	ADQ60192 Galanin/M
30	133	100.0	27	8	ADR00873 Transport
31	133	100.0	27	8	ADSI17605 Membrane
32	133	100.0	28	8	ADK39821 PNA molec
33	133	100.0	28	8	ADO57519 Transport
34	131	98.5	27	8	ADH89695 Cell pene
35	128	96.2	27	8	ADH89696 Cell pene
36	127	95.5	27	8	ADO25261 transpor
37	126	94.7	27	7	ADC22458
38	126	94.7	27	7	ADC22452 Protein-d
39	126	94.7	27	7	ADH76188
40	126	94.7	27	7	ADH76182 Transduct
41	126	94.7	27	8	ADH89702 Cell pene
42	126	94.7	27	8	ADI52969 Polyacch
43	126	94.7	27	8	ADLI4690 Cardiant
44	126	94.7	27	8	ADLI4684 Cardiant
45	126	94.7	27	8	ADR31976 Heat shoc

```
XX SQ Sequence 27 AA;
Query Match 100.0%; Score 133; DB 2; Length 27;
Best Local Similarity 100.0%; Pred. No. 2.5e-13;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GWTLSAGYLLGKINKLALAALAKKIL 27
| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 GWTLSAGYLLGKINKLALAALAKKIL 27

RESULT 2
AAB17999
ID AAB17999 standard; peptide; 27 AA.
XX
AC AAB17999;
XX
DT 31-OCT-2000 (first entry)
XX
DE Membrane transporting peptide sequence SEQ ID NO:1111.
XX
KW Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP;
KW inhibitor; erythropoietin; thrombopoietin; interleukin 1;
KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
KW vascular endothelial growth factor; matrix metalloproteinase; asthma;
KW thrombosis; pharmaceutical.
XX
OS Synthetic.
XX
PN WO200024782-A2.
XX
PD 04-MAY-2000.
XX
PF 25-OCT-1999; 99WO-US025044.
XX
PR 23-OCT-1998; 98US-0105371P.
PR 22-OCT-1999; 99US-00428082.
XX
PA (AMGE-) AMGEN INC.
XX
PI Feige U, Liu C, Cheetham J, Boone TC;
XX
DR WPI; 2000-350702/30.
XX
PT Novel composition of matter comprising an Fc domain and pharmacologically
PT active peptides, useful for treating cancer and autoimmune diseases.
XX
PS Disclosure; Page 602; 608pp; English.
XX
CC The present invention describes composition of matter (I) comprising an
CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
CC (X1)a-P1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-
CC (L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2,
CC P3, and P4 = are each independently sequences of pharmacologically active
CC peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b,
CC c, d, e, and f = are each independently 0 or 1, provided that at least 1
CC of a and b is 1. The composition can have cytostatic, antiasthmatic,
CC thrombolytic and immunosuppressive activities. DNAs, vectors and host
CC cells from the present invention can be used for producing pharmaceutical
CC compositions. The compositions are useful for treating cancer, asthma,
CC thrombosis, or autoimmune diseases. The use of an Fc domain (rather than
CC a Fab domain) can provide a longer half-life or incorporate functions
CC such as Fc receptor binding, protein A binding, complement fixation, and
CC possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to
CC AAB18003 represent nucleotide and amino acid sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 27 AA;
Query Match 100.0%; Score 133; DB 3; Length 27;
Best Local Similarity 100.0%; Pred. No. 2.5e-13;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GWTLSAGYLLGKINKLALAALAKKIL 27
| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 GWTLSAGYLLGKINKLALAALAKKIL 27

RESULT 3
AAB22024
ID AAB22024 standard; peptide; 27 AA.
XX
AC AAB22024;
XX
DT 08-JAN-2001 (first entry)
XX
DE Membrane penetrating peptide #1.
XX
KW Cystic fibrosis transmembrane conductance regulator; CFTR; CF;
KW chloride channel; membrane penetrating peptide.
XX
OS Unidentified.
XX
PN WO200050591-A1.
XX
PD 31-AUG-2000.
XX
PF 24-FEB-2000; 2000WO-US004642.
XX
PR 24-FEB-1999; 99US-0121495P.
XX
PA (UYCA-) UNIV CASE WESTERN RESERVE.
XX
PI Adams LM, Davis PB, Ma J;
XX
DR WPI; 2000-572090/53.
XX
PT Polypeptide useful for enhancing the open probability of cystic fibrosis
PT transmembrane conductance regulator chloride channel in cystic fibrosis
PT patients having minimally active mutant protein.
XX
PS Claim 5; Page 31; 35pp; English.
XX
CC Defects in the cystic fibrosis transmembrane conductance regulator
CC (CFTR), are associated with cystic fibrosis (CF). CFTR is a chloride
CC channel located in the apical membrane of epithelial cells. The present
CC invention relates to peptide fragments of human CFTR (see AAB22022 and
CC AAB22023), which are useful for CF therapy, in that they can activate and
CC open a CFTR protein by the formation of a cAMP regulated chloride
CC channel. The present peptide is a membrane penetrating peptide, which can
CC be fused onto the AAB22022 and AAB22023 peptides. The present peptide can
CC be used to facilitate the uptake of the AAB22022 and AAB22023 peptides by
CC target cells
XX
SQ Sequence 27 AA;
Query Match 100.0%; Score 133; DB 3; Length 27;
Best Local Similarity 100.0%; Pred. No. 2.5e-13;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GWTLSAGYLLGKINKLALAALAKKIL 27
| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 GWTLSAGYLLGKINKLALAALAKKIL 27

RESULT 4
AAB29575
ID AAB29575 standard; protein; 27 AA.
XX
AC AAB29575;
XX
DT 15-FEB-2001 (first entry)
```

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 4, 2005, 14:04:32 ; Search time 143.791 Seconds  
(without alignments)  
77.948 Million cell updates/sec

Title: US-10-071-512A-3

Perfect score: 133

Sequence: 1 GWTLSAGYLLGKINKALAAKIL 27

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1846076 seqs, 415116000 residues

Total number of hits satisfying chosen parameters: 1846076

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*
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- 9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*
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- 18: /cgn2\_6/ptodata/2/pubpaa/US10F\_NEW\_PUB.pep.\*
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- 22: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	133	100.0	27	10	US-09-948-193-18
2	133	100.0	27	10	US-09-295-189-5
3	133	100.0	27	12	US-09-777-560-12
4	133	100.0	27	14	US-10-071-512A-3
5	133	100.0	27	14	US-10-252-012-4
6	133	100.0	27	14	US-10-156-570A-25
7	133	100.0	27	14	US-10-201-394A-21
8	133	100.0	27	14	US-10-201-389A-21
9	133	100.0	27	15	US-10-144-549-16
10	133	100.0	27	15	US-10-357-529-9
11	133	100.0	27	15	US-10-232-410-13
12	133	100.0	27	10	US-09-948-193-18
13	133	100.0	27	10	US-09-295-189-5
14	133	100.0	27	12	US-09-777-560-12
15	133	100.0	27	14	US-10-071-512A-3
16	133	100.0	27	14	US-10-252-012-4
17	133	100.0	27	14	US-10-156-570A-25
18	133	100.0	27	14	US-10-201-394A-21
19	133	100.0	27	14	US-10-201-389A-21
20	133	100.0	27	15	US-10-144-549-16
21	133	100.0	27	15	US-10-357-529-9
22	133	100.0	27	15	US-10-232-410-13

12	133	100.0	27	15	US-10-609-217-1109	Sequence 1109, Ap
13	133	100.0	27	15	US-10-632-388-1109	Sequence 1109, Ap
14	133	100.0	27	15	US-10-357-826A-3	Sequence 3, Appli
15	133	100.0	27	15	US-10-651-723-1109	Sequence 1109, Ap
16	133	100.0	27	15	US-10-645-761-1109	Sequence 1109, Ap
17	133	100.0	27	15	US-10-261-161-24	Sequence 24, Appli
18	133	100.0	27	15	US-10-666-696-1109	Sequence 1109, Ap
19	133	100.0	27	15	US-10-653-048-1109	Sequence 1109, Ap
20	133	100.0	27	16	US-10-427-160A-21	Sequence 21, Appli
21	133	100.0	27	16	US-10-743-381-4	Sequence 4, Appli
22	133	100.0	27	16	US-10-751-380-20	Sequence 20, Appli
23	133	100.0	27	16	US-10-165-860A-4	Sequence 4, Appli
24	133	100.0	27	16	US-10-444-853A-514	Sequence 514, App
25	133	100.0	27	16	US-10-634-447-5	Sequence 5, Appli
26	133	100.0	27	16	US-10-780-447-21	Sequence 21, Appli
27	133	100.0	27	17	US-10-757-803-514	Sequence 514, App
28	133	100.0	27	17	US-10-826-966-514	Sequence 514, App
29	133	100.0	27	17	US-10-795-081A-12	Sequence 12, Appli
30	133	100.0	27	17	US-10-930-313-56	Sequence 56, Appli
31	133	100.0	27	18	US-10-645-784-1109	Sequence 1109, Ap
32	133	100.0	27	18	US-10-694-243-8	Sequence 8, Appli
33	133	100.0	27	18	US-10-972-963-8	Sequence 8, Appli
34	133	100.0	27	18	US-10-353-902-7	Sequence 7, Appli
35	133	100.0	27	18	US-10-878-175B-35	Sequence 35, Appli
36	133	100.0	27	20	US-11-001-674-12	Sequence 12, Appli
37	127	95.5	27	17	US-10-700-971C-3	Sequence 3, Appli
38	126	94.7	27	14	US-10-226-956-283	Sequence 283, App
39	126	94.7	27	14	US-10-226-956-289	Sequence 289, App
40	126	94.7	27	14	US-10-211-088-301	Sequence 301, App
41	126	94.7	27	14	US-10-211-088-307	Sequence 307, App
42	126	94.7	27	14	US-10-405-339-30	Sequence 30, Appli
43	116.5	87.6	26	9	US-09-785-802A-12	Sequence 12, Appli
44	116.5	87.6	26	10	US-09-965-876A-4	Sequence 4, Appli
45	116.5	87.6	26	14	US-10-077-555-10	Sequence 10, Appli

#### ALIGNMENTS

RESULT 1  
US-09-948-193-18  
; Sequence 18, Application US/09948193  
; Publication No. US20030027335A1  
; GENERAL INFORMATION:  
; APPLICANT: Jo, Daewoong  
; APPLICANT: Rulev, H. Earl  
; TITLE OF INVENTION: Genome Engineering by Cell-Permeable DNA  
; TITLE OF INVENTION: Site-Specific Recombinases  
; FILE REFERENCE: 22000.0109U2  
; CURRENT APPLICATION NUMBER: US/09/948,193  
; CURRENT FILING DATE: 2001-09-07  
; PRIOR APPLICATION NUMBER: 60/230,690  
; PRIOR FILING DATE: 2000-09-07  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 18  
; LENGTH: 27  
; TYPE: PXT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description: Transportan  
US-09-948-193-18

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Db 1 GWTLSAGYLLGKINKALAAKIL 27  
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RESULT 2

US-09-295-189-5  
; Sequence 5, Application US/09295189  
; Publication No. US20030083273A1  
; GENERAL INFORMATION:  
; APPLICANT: Woolf, Tod M.  
; TITLE OF INVENTION: Improved Antisense Oligomers  
; FILE REFERENCE: SRI-004  
; CURRENT APPLICATION NUMBER: US/09/295,189  
; CURRENT FILING DATE: 1999-04-20  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 27  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: construct  
US-09-295-189-5

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Best Local Similarity 100.0%; Pred. No. 2.7e-12;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GWTLSAGYLLGKINKLALAALAKKIL 27

RESULT 3  
US-09-777-560-12  
; Sequence 12, Application US/09777560  
; Publication No. US20050130884A1  
; GENERAL INFORMATION:  
; APPLICANT: BRANDT, CURTIS R.  
; TITLE OF INVENTION: PHARMACOLOGICALLY ACTIVE ANTIVIRAL PEPTIDES AND METHODS  
; FILE REFERENCE: 032026-0460  
; CURRENT APPLICATION NUMBER: US/09/777,560  
; CURRENT FILING DATE: 2001-02-06  
; PRIOR APPLICATION NUMBER: 60/184,057  
; PRIOR FILING DATE: 2000-02-22  
; PRIOR APPLICATION NUMBER: 60/180,823  
; PRIOR FILING DATE: 2000-02-07  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 12  
; LENGTH: 27  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
US-09-777-560-12

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Best Local Similarity 100.0%; Pred. No. 2.7e-12;  
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RESULT 4  
US-10-071-512A-3  
; Sequence 3, Application US/10071512A  
; Publication No. US20030031655A1  
; GENERAL INFORMATION:  
; APPLICANT: Woolf, Tod M.  
; TITLE OF INVENTION: METHODS OF LIGHT ACTIVATED RELEASE OF LIGANDS FROM  
; TITLE OF INVENTION: ENDOSOMES

; FILE REFERENCE: SRI-014  
; CURRENT APPLICATION NUMBER: US/10/071,512A  
; CURRENT FILING DATE: 2002-10-08  
; PRIOR APPLICATION NUMBER: US 60/267272  
; PRIOR FILING DATE: 2001-02-08  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 27  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic construct  
US-10-071-512A-3

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Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 5  
US-10-252-012-4  
; Sequence 4, Application US/10252012  
; Publication No. US20030100501A1  
; GENERAL INFORMATION:  
; APPLICANT: Davis, Pamela B.  
; TITLE OF INVENTION: OAN2NEG2 AN ACTIVATOR OF WILD TYPE AND MUTANT CFTR CHLORIDE CHANNEL  
; FILE REFERENCE: 03037.00012  
; CURRENT APPLICATION NUMBER: US/10/252,012  
; CURRENT FILING DATE: 2002-09-23  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 4  
; LENGTH: 27  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-10-252-012-4

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RESULT 6  
US-10-156-570A-25  
; Sequence 25, Application US/10156570A  
; Publication No. US20030125242A1  
; GENERAL INFORMATION:  
; APPLICANT: ROSENECKER, JOSEPH  
; APPLICANT: RITTER, WOLFGANG  
; APPLICANT: RUDOLPH, CARSTEN MARTIN  
; APPLICANT: PLANK, CHRISTIAN  
; TITLE OF INVENTION: POLYPEPTIDES COMPRISING MULTIMERS OF NUCLEAR  
; TITLE OF INVENTION: LOCALIZATION SIGNALS OR OF PROTEIN TRANSDUCTION DOMAINS  
; TITLE OF INVENTION: AND THEIR USE FOR TRANSFERRING NUCLEIC ACID MOLECULES  
; FILE REFERENCE: INTO CELLS  
; FILE REFERENCE: VOS-35  
; CURRENT APPLICATION NUMBER: US/10/156,570A  
; CURRENT FILING DATE: 2002-05-24  
; PRIOR APPLICATION NUMBER: PCT/EP00/11690  
; PRIOR FILING DATE: 2000-11-23  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn ver. 2.1  
; SEQ ID NO 25

GenCore version 5.1.1.6  
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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	133	100.0	27	1	PCT-US02-22324-21	Sequence 21, Appl
2	133	100.0	27	1	PCT-US02-30094-4	Sequence 4, Appl
3	133	100.0	27	1	PCT-US03-25567-64	Sequence 64, Appl
4	133	100.0	27	1	PCT-US03-28092-24	Sequence 24, Appl
5	133	100.0	27	1	PCT-US03-33801-8	Sequence 8, Appl
6	133	100.0	27	1	PCT-US03-34424-29	Sequence 29, Appl
7	133	100.0	27	1	PCT-US03-34686-26	Sequence 26, Appl
8	133	100.0	27	1	PCT-US04-11195-112	Sequence 112, Appl
9	133	100.0	27	1	PCT-US04-35137-8	Sequence 8, Appl
10	133	100.0	27	1	PCT-US99-25044-1111	Sequence 1111, Ap
11	133	100.0	27	16	US-09-295-189-5	Sequence 5, Appl
12	133	100.0	27	19	US-09-563-286B-1109	Sequence 1109, Ap
13	133	100.0	27	19	US-09-563-286C-1109	Sequence 1109, Ap
14	133	100.0	27	22	US-09-777-560-12	Sequence 12, Appl
15	133	100.0	27	24	US-09-914-213-4	Sequence 4, Appl
16	133	100.0	27	24	US-09-948-193-18	Sequence 18, Appl
17	133	100.0	27	26	US-10-071-512A-3	Sequence 3, Appl
18	133	100.0	27	27	US-10-156-570A-25	Sequence 25, Appl
19	133	100.0	27	27	US-10-185-860A-4	Sequence 4, Appl
20	133	100.0	27	28	US-10-201-389A-21	Sequence 21, Appl
21	133	100.0	27	28	US-10-201-394A-21	Sequence 21, Appl
22	133	100.0	27	28	US-10-232-410-13	Sequence 13, Appl
23	133	100.0	27	28	US-10-252-012-4	Sequence 4, Appl
24	133	100.0	27	28	US-10-261-161-24	Sequence 24, Appl
25	133	100.0	27	29	US-10-353-902-7	Sequence 7, Appl
26	133	100.0	27	29	US-10-357-529-9	Sequence 9, Appl
27	133	100.0	27	29	US-10-357-826A-3	Sequence 3, Appl
28	133	100.0	27	30	US-10-427-160A-21	Sequence 21, Appl
29	133	100.0	27	30	US-10-444-853A-514	Sequence 514, App
30	133	100.0	27	32	US-10-609-217-1109	Sequence 1109, Ap
31	133	100.0	27	32	US-10-624-447-5	Sequence 5, Appl
32	133	100.0	27	32	US-10-632-388-1109	Sequence 1109, Ap
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36	133	100.0	27	32	US-10-653-048-1109	Sequence 1109, Ap
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41	133	100.0	27	33	US-10-757-803-514	Sequence 514, App
42	133	100.0	27	33	US-10-780-447-21	Sequence 21, Appl
43	133	100.0	27	33	US-10-795-881A-12	Sequence 12, Appl
44	133	100.0	27	34	US-10-826-966-514	Sequence 514, App
45	133	100.0	27	34	US-10-874-920-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1  
PCT-US02-22324-21  
; Sequence 21, Application PC/TUS0222324  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc  
; APPLICANT: Beigelman, Leonid  
; APPLICANT: Azharyev, Alex  
; APPLICANT: Azharyeva, Elena  
; APPLICANT: Antopol'sky, Maxim  
; TITLE OF INVENTION: ENZYMAIC NUCLEIC ACID PEPTIDE CONJUGATES  
; FILE REFERENCE: MBH01-895-B (600/024)  
; CURRENT APPLICATION NUMBER: PCT/US02/22324  
; CURRENT FILING DATE: 2002-07-02  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 21  
; LENGTH: 27  
; TYPE: PRT  
; ORGANISM: Artificial Sequence

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; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Synthetic peptide
PCT-US02-22324-21

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Best Local Similarity 100.0%; Pred. No. 2.4e-13;
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Db 1 GWTLSAGYLLGKINKLALAALAKKIL 27

RESULT 2
PCT-US02-30094-4
; Sequence 4, Application PC/TUS0230094
; GENERAL INFORMATION:
; APPLICANT: Davis, Pamela B.
; TITLE OF INVENTION: QAN2NEG2 AN ACTIVATOR OF WILD TYPE AND MUTANT CFTR CHLORIDE CHANNEL
; FILE REFERENCE: 03037.000011
; CURRENT APPLICATION NUMBER: PCT/US02/30094
; CURRENT FILING DATE: 2002-09-23
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 27
; TYPE: PRT
; ORGANISM: homo sapiens
PCT-US02-30094-4

Query Match      100.0%; Score 133; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 2.4e-13;
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Db 1 GWTLSAGYLLGKINKLALAALAKKIL 27

RESULT 3
PCT-US03-25567-64
; Sequence 64, Application PC/TUS0325567
; GENERAL INFORMATION:
; APPLICANT: ISIS Pharmaceuticals, Inc.
; TITLE OF INVENTION: Novel Peptide-Conjugated Oligomeric Compounds
; FILE REFERENCE: ISIS-5244
; CURRENT APPLICATION NUMBER: PCT/US03/25567
; CURRENT FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: US 10/222,595
; PRIOR FILING DATE: 2002-08-16
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 64
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
PCT-US03-25567-64

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RESULT 4
PCT-US03-28092-24
; Sequence 24, Application PC/TUS0328092
; GENERAL INFORMATION:
; APPLICANT: Allergan, Inc.
; TITLE OF INVENTION: Cell-Based Fluorescence Resonance Energy Transfer (FRET) Assays For Clostridial Toxins
; FILE REFERENCE: 17511 (BOT)
; CURRENT APPLICATION NUMBER: PCT/US03/28092
; CURRENT FILING DATE: 2003-09-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
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Db 1 GWTLSAGYLLGKINKLALAALAKKIL 27

RESULT 5
PCT-US03-33801-8
; Sequence 8, Application PC/TUS0333801
; GENERAL INFORMATION:
; APPLICANT: GEORGIA TECH RESEARCH CORPORATION
; APPLICANT: EMORY UNIVERSITY
; TITLE OF INVENTION: MULTIFUNCTIONAL MAGNETIC NANOPARTICLE PROBES FOR INTRACELLULAR MOLECULAR IMAGING AND MONITORING
; FILE REFERENCE: 17625-0059
; CURRENT APPLICATION NUMBER: PCT/US03/33801
; CURRENT FILING DATE: 2003-10-27
; PRIOR APPLICATION NUMBER: 60/421,361
; PRIOR FILING DATE: 2002-10-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 8
; LENGTH: 27
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; ORGANISM: Artificial Sequence
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
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Best Local Similarity 100.0%; Pred. No. 2.4e-13;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GWTLSAGYLLGKINKLALAALAKKIL 27

RESULT 6
PCT-US03-34424-29
; Sequence 29, Application PC/TUS0334424
; GENERAL INFORMATION:
; APPLICANT: The Center For Blood Research, Inc., et al.
; TITLE OF INVENTION: INHIBITION OF GENE EXPRESSION USING RNA INTERFERING AGENTS
; FILE REFERENCE: CBN-007PC
; CURRENT APPLICATION NUMBER: PCT/US03/34424
; CURRENT FILING DATE: 2003-10-29
; PRIOR APPLICATION NUMBER: 60/422,419
; PRIOR FILING DATE: 2002-10-29
; NUMBER OF SEQ ID NOS: 31
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GenCore version 5.1.6  
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Title: US-10-071-512A-3

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#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	133	100.0	27	1	PCT-US05-05458-12
4	133	100.0	27	1	PCT-US04-36200-10
5	133	100.0	27	1	PCT-US04-40119-12
6	133	100.0	27	1	PCT-US04-06911A-12
7	133	100.0	27	6	US-10-930-313-56
8	133	100.0	27	6	US-10-156-570B-25
9	133	100.0	27	6	US-10-909-769-3
10	133	100.0	27	6	US-10-878-175B-35
11	133	100.0	27	6	US-10-201-389B-21
12	133	100.0	27	6	US-10-535-780-4
13	133	100.0	27	6	US-10-923-112A-35
14	133	100.0	27	7	US-11-041-103-7
15	133	100.0	27	7	US-11-109-015-2
16	133	100.0	27	7	US-11-001-674-12
17	133	100.0	27	7	US-11-067-092A-7
18	133	100.0	27	7	US-11-126-562-9
19	133	100.0	27	7	US-11-126-551-9
20	133	100.0	27	7	US-11-049-636-16
21	133	100.0	27	7	US-11-112-950-3
22	133	100.0	27	7	US-11-107-371-3
23	133	100.0	27	8	US-60-654-981-11
24	133	100.0	27	8	US-60-654-981-23
25	127	95.5	27	1	PCT-US05-16746-3

26 127 95.5 27 6 US-10-700-971C-3 Sequence 3, Appli  
27 126 94.7 27 7 US-11-078-256-283 Sequence 283, App  
28 126 94.7 27 7 US-11-078-256-283 Sequence 289, App  
29 116.5 87.6 26 6 US-10-991-286A-35 Sequence 35, Appl  
30 116.5 87.6 26 6 US-10-985-425-5 Sequence 5, Appl  
31 116.5 87.6 26 6 US-10-899-912A-28 Sequence 28, Appl  
32 116.5 87.6 26 7 US-11-016-542-7 Sequence 7, Appl  
33 112 84.2 25 7 US-11-126-562-11 Sequence 11, Appl  
34 112 84.2 25 7 US-11-126-551-11 Sequence 11, Appl  
35 112 84.2 25 8 US-60-654-981-26 Sequence 26, Appl  
36 111 83.5 24 7 US-11-126-562-10 Sequence 10, Appl  
37 111 83.5 24 7 US-11-126-551-10 Sequence 10, Appl  
38 111 83.5 24 8 US-60-654-981-24 Sequence 24, Appl  
39 97 72.9 21 1 PCT-US05-18995-18 Sequence 18, Appl  
40 97 72.9 21 1 PCT-US04-06911A-13 Sequence 13, Appl  
41 97 72.9 21 7 US-11-126-562-12 Sequence 12, Appl  
42 97 72.9 21 7 US-11-126-551-12 Sequence 12, Appl  
43 97 72.9 21 7 US-11-141-725-15 Sequence 15, Appl  
44 97 72.9 21 8 US-60-654-981-27 Sequence 27, Appl  
45 90 67.7 22 7 US-11-126-562-13 Sequence 13, Appl

#### ALIGNMENTS

RESULT 1  
PCT-US04-35009-6  
; Sequence 6, Application PC/TUS0435009  
; GENERAL INFORMATION:  
; APPLICANT: Wake Forest University Health Sciences  
; APPLICANT: Payne, R. Mark  
; TITLE OF INVENTION: NON-VIRAL DELIVERY OF COMPOUNDS TO THE MITOCHONDRIA  
; FILE REFERENCE: 9151-37W0  
; CURRENT APPLICATION NUMBER: PCT/US04/35009  
; CURRENT FILING DATE: 2004-10-22  
; PRIOR APPLICATION NUMBER: US 60/514,892  
; PRIOR FILING DATE: 2003-10-24  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 6  
; LENGTH: 27  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Synthetic PTD sequence  
PCT-US04-35009-6

Query Match 100.0%; Score 133; DB 1; Length 27;  
Best Local Similarity 100.0%; Pred. No. 5.1e-13;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GWTLSAGYLLGKINLKALALAKKIL 27  
|||||

Db 1 GWTLSAGYLLGKINLKALALAKKIL 27  
|||||

#### RESULT 2

PCT-US05-01771-7  
; Sequence 7, Application PC/TUS0501771  
; GENERAL INFORMATION:  
; APPLICANT: Georgia Tech Research Corporation  
; APPLICANT: Bao, Gang  
; APPLICANT: Nitin, Nitin  
; TITLE OF INVENTION: Activatable Probes and Methods For In Vivo Gene Detection  
; FILE REFERENCE: 820701-2820  
; CURRENT APPLICATION NUMBER: PCT/US05/01771  
; CURRENT FILING DATE: 2005-01-28  
; PRIOR APPLICATION NUMBER: 10/179,730  
; PRIOR FILING DATE: 2002-06-25  
; PRIOR APPLICATION NUMBER: 60/300,672  
; PRIOR FILING DATE: 2001-06-25  
; PRIOR APPLICATION NUMBER: 60/303,258  
; PRIOR FILING DATE: 2001-07-03

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; PRIOR APPLICATION NUMBER: 60/538,381
; PRIOR FILING DATE: 2004-01-21
; PRIOR APPLICATION NUMBER: 60/538,382
; PRIOR FILING DATE: 2004-01-21
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 7
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Protein Transduction Domain
PCT-US05-01771-7

Query Match      100.0%; Score 133; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 5.1e-13;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GWTLSAGYLLGKINLKALAALAKKIL 27
Db 1 GWTLSAGYLLGKINLKALAALAKKIL 27

RESULT 3
PCT-US05-05458-12
; Sequence 12, Application PC/TUS050505458
; GENERAL INFORMATION:
; APPLICANT: Dana-Farber Cancer Institute, Inc., et al.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
; FILE REFERENCE: DFN-058PC
; CURRENT APPLICATION NUMBER: PCT/US05/05458
; CURRENT FILING DATE: 2005-03-02
; PRIOR APPLICATION NUMBER: 60/548,139
; PRIOR FILING DATE: 2004-02-25
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
PCT-US05-05458-12

Query Match      100.0%; Score 133; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 5.1e-13;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GWTLSAGYLLGKINLKALAALAKKIL 27
Db 1 GWTLSAGYLLGKINLKALAALAKKIL 27

RESULT 4
PCT-US04-36200-10
; Sequence 10, Application PC/TUS0436200
; GENERAL INFORMATION:
; APPLICANT: THE CBR INSTITUTE FOR BIOMEDICAL RESEARCH, INC.
; APPLICANT: LIEBERMAN, JUDY
; APPLICANT: HAMAR, PETER
; TITLE OF INVENTION: METHODS FOR TREATING AND PREVENTING ISCHEMIA-REPERFUSION
; FILE REFERENCE: 033393-55221
; CURRENT APPLICATION NUMBER: PCT/US04/36200
; CURRENT FILING DATE: 2004-11-01
; PRIOR APPLICATION NUMBER: 60/516,172
; PRIOR FILING DATE: 2003-10-30
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patent in ver. 3.2
; SEQ ID NO 10
; LENGTH: 27
; TYPE: PRT
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; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Transportan A
PCT-US04-36200-10

Query Match      100.0%; Score 133; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 5.1e-13;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GWTLSAGYLLGKINLKALAALAKKIL 27
Db 1 GWTLSAGYLLGKINLKALAALAKKIL 27

RESULT 5
PCT-US04-40119-12
; Sequence 12, Application PC/TUS0440119
; GENERAL INFORMATION:
; APPLICANT: BRANDT, CURTIS R.
; APPLICANT: BULTMANN, HERMANN
; TITLE OF INVENTION: PEPTIDES AND METHODS FOR INDUCING CELLULAR RESISTANCE
; FILE REFERENCE: 032026-0827
; CURRENT APPLICATION NUMBER: PCT/US04/40119
; CURRENT FILING DATE: 2004-12-01
; PRIOR APPLICATION NUMBER: 60/526,252
; PRIOR FILING DATE: 2003-12-01
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patent in Ver. 3.3
; SEQ ID NO 12
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
PCT-US04-40119-12

Query Match      100.0%; Score 133; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 5.1e-13;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GWTLSAGYLLGKINLKALAALAKKIL 27
Db 1 GWTLSAGYLLGKINLKALAALAKKIL 27

RESULT 6
PCT-US04-06911A-12
; Sequence 12, Application PC/TUS0406911A
; GENERAL INFORMATION:
; APPLICANT: Kohler, Heinz
; TITLE OF INVENTION: TRANS-MEMBRANE-ANTIBODY INDUCED INHIBITION OF APOPTOSIS
; FILE REFERENCE: 411.35629AP3
; CURRENT APPLICATION NUMBER: PCT/US04/06911A
; CURRENT FILING DATE: 2004-03-05
; PRIOR APPLICATION NUMBER: 60/451,980
; PRIOR FILING DATE: 2003-03-05
; PRIOR APPLICATION NUMBER: 09/865,281
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 09/070,907
; PRIOR FILING DATE: 1998-05-04
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 12
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Synthesized peptide
PCT-US04-06911A-12
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 4, 2005, 14:20:28 ; Search time 31.3953 Seconds  
(without alignments)  
82.746 Million cell updates/sec

Title: US-10-071-512A-3  
Perfect score: 133  
Sequence: 1 GWTLSAGYLLGKLNKALAKKIL 27  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_79:.\*  
1: pir1:.\*  
2: pir2:.\*  
3: pir3:.\*  
4: pir4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	67	50.4	29	S17147	galanin - chicken
2	67	50.4	99	S34301	galanin - mouse
3	67	50.4	123	RHBOG	galanin precursor
4	67	50.4	123	RHHUN	galanin precursor
5	67	50.4	123	RHPGN	galanin precursor
6	67	50.4	124	RHRTN	galanin precursor
7	67	50.4	124	JCS480	galanin precursor
8	61	45.9	14	QMWAVV	mastoparan - yello
9	57	42.9	14	QMVHMM	mastoparan M - hor
10	55	41.4	558	T47505	hypothetical prote
11	54	40.6	14	JN0389	histamine-releasin
12	52	39.1	516	T47509	probable transport
13	52	39.1	548	T47510	probable transport
14	52	39.1	555	T47512	probable transport
15	51	38.3	14	QMVHP2	mastoparan C - Eur
16	51	38.3	558	T47508	probable transport
17	50	37.6	557	T47506	hypothetical prote
18	50	37.6	609	T00904	hypothetical prote
19	50	37.6	1260	T04440	hypothetical prote
20	49.5	37.2	167	AG3384	3-dehydroquinat d
21	49	36.8	206	G83854	hypothetical prote
22	49	36.8	299	F90741	hypothetical prote
23	49	36.8	299	A85592	hypothetical prote
24	49	36.8	302	T09321	EPLF2 protein - hu
25	49	36.8	308	H64819	formate acetyltran
26	49	36.8	568	E70962	probable fadE4 pro
27	49	36.8	752	KXRTC1	proprotein convert
28	49	36.8	753	KXHUC1	proprotein convert
29	49	36.8	753	KXMSC1	proprotein convert

30	49	36.8	753	2	S59959	proprotein convert
31	48.5	36.5	426	2	A11177	3-hydroxy-3-methyl
32	48	36.1	219	2	G90602	chromate transport
33	47.5	35.7	426	2	AE1535	3-hydroxy-3-methyl
34	47	35.3	105	1	RSUC12	ribosomal protein
35	47	35.3	190	2	D75006	hypothetical prote
36	47	35.3	326	2	AB2810	hypothetical prote
37	47	35.3	326	2	E97588	bifunctional carbo
38	47	35.3	438	2	C72006	conserved hypoteth
39	47	35.3	438	2	F86619	CT372 hypotethical
40	47	35.3	2971	2	T08026	hypothetical prote
41	46.5	35.0	226	2	C69760	amino acid ABC tra
42	46.5	35.0	350	2	JN0621	G protein-coupled
43	46.5	35.0	374	2	F81693	iron-sulfur cofact
44	46	34.6	122	2	H70791	hypothetical prote
45	46	34.6	201	2	AG0793	Ais protein (impor

ALIGNMENTS

RESULT 1

S17147  
galanin - chicken (fragment)  
C:Species: Gallus gallus (chicken)  
C:Date: 21-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 09-Jul-2004  
C:Accession: S17147  
R:Norberg, A.; Sillard, R.; Carlquist, M.; Joernvall, H.; Mutt, V.  
FEBS Lett. 288, 151-153, 1991  
A:Title: Chemical detection of natural peptides by specific structures. Isolation of chi  
A:Reference number: S17147; MUID:91348254; PMID:1715289  
A:Accession: S17147  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-29 <NOR>  
A:Cross-references: UNIPROT:P30802  
C:Superfamily: galanin

Query Match 50.4%; Score 67; DB 2; Length 29;  
Best Local Similarity 100.0%; Pred. No. 0.003;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GWTLSAGYLLG 12  
Db 1 GWTLSAGYLLG 12  
|||||  
|||||

RESULT 2

S34301  
galanin - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004  
C:Accession: S34301  
R:Land, T.; Lundqvist, J.; Bartfai, T.  
submitted to the EMBL Data Library, June 1993  
A:Description: Cloning of mouse galanin/cDNA.  
A:Reference number: S34301  
A:Accession: S34301  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-99 <LAN>  
A:Cross-references: UNIPROT:P47212; EMBL:Z23069; NID:g312338; PIDN:CAA80610.1; PID:g31233  
C:Superfamily: galanin

Query Match 50.4%; Score 67; DB 2; Length 99;  
Best Local Similarity 100.0%; Pred. No. 0.011;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GWTLSAGYLLG 12  
Db 8 GWTLSAGYLLG 19  
|||||  
|||||

```

RESULT 3
RHBOG
galanin precursor - bovine
C:Species: Bos primigenius taurus (cattle)
C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C:Accession: S01011; I46971
R:Roekaeus, A.; Carlquist, M.
FEBS Lett. 234, 400-406, 1988
A>Title: Nucleotide sequence analysis of cDNAs encoding a bovine galanin precursor protein
A:Reference number: S01011; MUID:88271665; PMID:2455659
A:Molecule type: mRNA
A:Residues: 1-123 <ROB>
A:Cross-references: UNIPROT:P11242; EMBL:X12582; NID:G376; PIDN:CAA31094.1; PID:G377
A>Note: the authors translated the codon ACT for residue 95 as Tyr
R:Anouar, Y.; MacArthur, L.; Cohen, J.; Iacangelo, A.L.; Eiden, L.E.
J. Biol. Chem. 269, 6823-6831, 1994
A>Title: Identification of a TPA-responsive element mediating preferential transactivation
A:Reference number: I46971; MUID:94165083; PMID:7509811
A:Accession: I46971
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-27 <ANO>
A:Cross-references: GB:S68957; NID:G545739; PIDN:AAD14027.1; PID:G4261727
C:Superfamily: galanin
C:Keywords: amidated carboxyl end; hormone; intestine; neuropeptide
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-32/Domain: amino-terminal propeptide #status predicted <PRO>
F:33-61/Product: galanin #status predicted <MAT>
F:62-123/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F:61/Modified site: amidated carboxyl end (Ala) (amide in mature form from following gly

Query Match 50.4%; Score 67; DB 1; Length 123;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GWTLSAGYLLG 12
DB 33 GWTLSAGYLLG 44

RESULT 4
RHUN
galanin precursor [validated] - human
N:Contains: galanin; galanin mRNA associated peptide (GMAP)
C:Species: Homo sapiens (man)
C>Date: 31-Dec-1992 #sequence_revision 23-Mar-1995 #text_change 09-Jul-2004
C:Accession: A49353; A61116; A49154; A41630; S15931
R:Evans, H.; Baumgartner, M.; Shine, J.; Herzog, H.
Genomics 18, 473-477, 1993
A>Title: Genomic organization and localization of the gene encoding human preprogalanin.
A:Reference number: A49353; MUID:94140342; PMID:7508413
A:Accession: A49353
A:Molecule type: DNA
A:Residues: 1-45 <EV2>
A:Cross-references: UNIPROT:P22466; GB:L11144; NID:G306764; PIDN:AAA18248.1; PID:G488849
A>Note: neither nucleotide sequence nor translation is complete
R:Evans, H.F.; Shine, J.
Endocrinology 129, 1682-1684, 1991
A>Title: Human galanin: molecular cloning reveals a unique structure.
A:Reference number: A61116; MUID:91339793; PMID:1714839
A:Accession: A61116
A:Molecule type: mRNA
A:Residues: 1-123 <EVA>
R:McKnight, G.L.; Karlsson, A.E.; Kowalyk, S.; Mathewes, S.L.; Sheppard, P.O.; O'Hara, P.
Diabetes 41, 82-87, 1992
A>Title: Sequence of human galanin and its inhibition of glucose-stimulated insulin secretion
A:Reference number: A49154; MUID:92090542; PMID:1370155
A:Accession: A49154
A:Molecule type: mRNA
A:Residues: 17-123 <MCK>
A:Cross-references: GB:JM77140; NID:G190411; PIDN:AAA60178.1; PID:G190412
A>Note: sequence extracted from NCBI backbone (NCBIN:71608, NCBIP:71609)

```

```

R:Schmidt, W.E.; Kratzin, H.; Eckart, K.; Dreys, D.; Mundkowski, G.; Clemens, A.; Katson
Proc. Natl. Acad. Sci. U.S.A. 88, 11435-11439, 1991
A>Title: Isolation and primary structure of pituitary human galanin, a 30-residue nonam
A:Reference number: A41630; MUID:92107965; PMID:1722333
A:Accession: A41630
A:Molecule type: protein
A:Residues: 33-62 <SCH>
A>Note: sequence extracted from NCBI backbone
R:Bersani, M.; Johnsen, A.H.; Hojrup, P.; Dunning, B.E.; Andreassen, J.J.; Holst, J.J.
FEBS Lett. 283, 189-194, 1991
A>Title: Human galanin: primary structure and identification of two molecular forms.
A:Reference number: S15831; MUID:91257299; PMID:1710578
A:Accession: S15831
A:Molecule type: protein
A:Residues: 33-62 <BER>
A>Note: a form containing only the first nineteen residues of this sequence was also fou
C:Comment: This peptide causes smooth muscle contraction in the gastrointestinal tract a
C:Comment: This peptide in human differs from the pig, rat, and bovine forms by the absen
C:Genetics:
A:Gene: GDB:GALN
A:Cross-references: GDB:I41567; OMIM:137035
A:Map position: 11q13.3-11q13.5
C:Superfamily: galanin
F:1-23/Domain: signal sequence #status predicted <SIG>
F:33-62/Product: galanin #status experimental <MAT>
F:65-123/Product: galanin mRNA associated peptide (GMAP) #status predicted <RMAT>

Query Match 50.4%; Score 67; DB 1; Length 123;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GWTLSAGYLLG 12
DB 33 GWTLSAGYLLG 44

RESULT 5
RHFGN
galanin precursor - pig
N:Contains: preprogalanin, 7-residue amino end-extended form; preprogalanin, 9-residue a
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 30-Sep-1988 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
C:Accession: A23540; J00002; A49161
R:Roekaeus, A.; Brownstein, M.J.
Proc. Natl. Acad. Sci. U.S.A. 83, 6287-6291, 1986
A>Title: Construction of a porcine adrenal medullary cDNA library and nucleotide sequenc
A:Reference number: A23540; MUID:86313566; PMID:2428032
A:Accession: A23540
A:Molecule type: mRNA
A:Residues: 1-123 <ROB>
A:Cross-references: UNIPROT:P07480; GB:M13826; NID:G164605; PIDN:AAA31097.1; PID:G164606
R:Tatemoto, K.; Roekaeus, A.; Jornvall, H.; McDonald, T.J.; Mutt, V.
FEBS Lett. 164, 124-128, 1983
A>Title: Galanin: a novel biologically active peptide from porcine intestine.
A:Reference number: J00002; MUID:84085072; PMID:6197320
A:Accession: J00002
A:Molecule type: protein
A:Residues: 33-61 <TAT>
R:Bersani, M.; Thim, L.; Rasmussen, T.N.; Holst, J.J.
Endocrinology 129, 2693-2698, 1991
A>Title: Galanin and galanin extended at the N-terminus with seven and nine amino acids
A:Reference number: A49161; MUID:92037394; PMID:1718731
A:Accession: A49161
A:Molecule type: protein
A:Residues: 1-123 <BER>
A:Experimental source: adrenal medulla
A>Note: sequence extracted from NCBI backbone (NCBIP:63296)
C:Comment: This peptide contracts smooth muscle preparations from rat and causes a mild
C:Superfamily: galanin
F:1-23/Domain: amidated carboxyl end; hormone; intestine; neuropeptide

```

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 4, 2005, 14:08:33 ; Search time 145.674 Seconds  
(without alignments)  
94.911 Million cell updates/sec

Title: US-10-071-512A-3  
Perfect score: 133  
Sequence: 1 GWTLSAGVLLGKLNKALAALAKKIL 27

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt 03:\*

1: uniprot\_prot:\*  
2: uniprot\_tmbl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	69.5	52.3	115	1 GALP RAT	Q9qxg6 rattus norv
2	69	51.9	29	1 GALA_ONCMY	P47213 oncorhynch
3	69	51.9	55	2 Q8VIL6	Q8vile mus musculu
4	69	51.9	115	2 Q8SQD7	Q8sqd7 macaca neme
5	69	51.9	116	1 GALP HUMAN	Q9ubc7 homo sapien
6	69	51.9	117	2 Q810H5	Q810h5 mus musculu
7	69	51.9	120	1 GALP_PIG	Q9tt95 sus scrofa
8	68	51.1	58	2 Q7ZT95	Q7zt95 carassius a
9	68	51.1	81	2 Q7ZT97	Q7zt97 carassius a
10	68	51.1	95	2 Q7ZT92	Q7zt92 carassius a
11	68	51.1	118	2 Q7ZT94	Q7zt94 carassius a
12	67	50.4	26	2 Q7ZT98	Q7zt98 carassius a
13	67	50.4	29	1 GALA_ALLMI	P47215 alligator m
14	67	50.4	29	1 GALA_AMICA	P47214 amia calva
15	67	50.4	29	1 GALA_CHICK	P30802 gallus gall
16	67	50.4	29	1 GALA_RANRI	P47216 rana ridibu
17	67	50.4	29	1 GALA_SHEEP	P31234 ovis aries
18	67	50.4	50	2 Q7ZT89	Q7zt89 carassius a
19	67	50.4	55	2 Q8SQD6	Q8sqd6 macaca neme
20	67	50.4	81	2 Q7ZT96	Q7zt96 carassius a
21	67	50.4	117	1 GALA_COTJA	Q9w6m9 coturnix co
22	67	50.4	120	2 Q7ZT91	Q7zt91 carassius a
23	67	50.4	123	1 GALA_BOVIN	P11242 bos taurus
24	67	50.4	123	1 GALA_HUMAN	P22466 homo sapien
25	67	50.4	123	1 GALA_PIG	P07480 sus scrofa
26	67	50.4	124	1 GALA_MOUSE	P47212 mus musculu
27	67	50.4	124	1 GALA_RAT	P10683 rattus norv
28	67	50.4	142	2 Q7ZT93	Q7zt93 carassius a
29	67	50.4	144	2 Q7ZT90	Q7zt90 carassius a
30	61	45.9	14	1 MAST_VESLE	P01514 vespula lew
31	57	42.9	14	1 MAST_VESMA	P04205 vespa manda

32	55	41.4	558	2	Q9M1E2	Q9mie2 arabidopsis
33	54	40.6	14	1	MAST_VESOR	P17238 vespa orien
34	54	40.6	375	2	Q6L3J3	Q6l3j3 solanum dem
35	53.5	40.2	539	2	Q7NTF4	Q7ntf4 chromobacte
36	52	39.1	516	2	Q9M174	Q9mi74 arabidopsis
37	52	39.1	548	2	Q8GZ59	Q8gz59 arabidopsis
38	52	39.1	548	2	Q9M173	Q9mi73 arabidopsis
39	52	39.1	555	2	Q9M171	Q9mi71 arabidopsis
40	52	39.1	774	2	Q9YHY5	Q9yhy5 xenopus lae
41	52	39.1	1109	2	Q6BZH6	Q6bzh6 debaryomyce
42	51.5	38.7	589	2	Q7P6I6	Q7p6i6 fusobacteri
43	51	38.3	14	1	MAST_VESCR	P01516 vespa crabr
44	51	38.3	309	2	Q9AXI9	Q9axi9 oryza sativ
45	51	38.3	558	2	Q8GYF8	Q8gyf8 arabidopsis

#### ALIGNMENTS

RESULT 1

ID	GALP RAT	STANDARD	PRT	115 AA
AC	Q9QXG6			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	Galanin-like peptide precursor.			
OS	Name=Galp;			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_TaxID=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20069685; PubMed=10601261; DOI=10.1074/jbc.274.52.37041;			
RA	Ohtaki T., Kumano S., Ishibashi Y., Ogi K., Matsui H., Harada M.,			
RA	Kitada C., Kurokawa T., Onda H., Fujino M.;			
RT	"Isolation and cDNA cloning of a novel galanin-like peptide (GALP)			
RT	from porcine hypothalamus";			
RL	J. Biol. Chem. 274:37041-37045(1999).			
CC	- SUBCELLULAR LOCATION: Secreted.			
CC	- SIMILARITY: Belongs to the galanin family.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; AF108491; AAF19723.1; --			
DR	InterPro; IPR008174; Galanin.			
DR	Pfam; PF01296; Galanin; 1.			
DR	PROSITE; PS00861; GALANIN; 1.			
KW	Cleavage on pair of basic residues; Hormone; Neuropeptide; Signal.			
FT	SIGNAL 1 23 By similarity.			
FT	CHAIN 24 83 Galanin-like peptide.			
FT	PROPEP 86 115 By similarity.			
SEQ	SEQUENCE 115 AA; 12599 MW; 00BD3A2336AD06C5 CRC64;			
	Query Match 52.3%; Score 69.5; DB 1; Length 115;			
	Best Local Similarity 57.7%; Pred. No. 0 032;			
	Matches 15; Conservative 4; Mismatches 6; Indels 1; Gaps 1;			
QY	1 GWTLSAGVLLGKI-NLKALAALAKK 25			
	: : : : : :			
Db	32 GWTLSAGVLLGVLHLSKANQGRK 57			
RESULT 2				
ID	GALA_ONCMY	STANDARD	PRT	29 AA

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AC P47213;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Galanin.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE.
RC TISSUE=Stomach;
RX MEDLINE=95164756; PubMed=7532194;
RA Anglade I., Wang Y., Jensen J., Framu G., Kah O., Conlon J.M.;
RT "Characterization of trout galanin and its distribution in trout brain
RT and pituitary.";
RL J. Comp. Neurol. 350:63-74(1994).
CC -!- FUNCTION: Contracts smooth muscle of the gastrointestinal and
CC genitourinary tract, regulates growth hormone release, modulates
CC insulin release, and may be involved in the control of adrenal
CC secretion.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the galanin family.
DR InterPro; IPR008174; Galanin.
DR Pfam; PF01296; Galanin; 1.
DR PRINTS; PR00273; GALANIN.
DR ProDom; PD005962; Galanin; 1.
DR PROSITE; PS00861; GALANIN; 1.
KW Amidation; Direct protein sequencing; Hormone; Neuropeptide.
FT MOD_RES 29 29 Alanine amide.
SQ SEQUENCE 29 AA; 3044 MW; 73C37190403FA349 CRC64;

Query Match 51.9%; Score 69; DB 1; Length 29;
Best Local Similarity 56.0%; Pred. No. 0.011;
Matches 14; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

QY 1 GWTLSAGYLLGKINLKALAAAKK 25
Db ||||| :
1 GWTLSAGYLLGPHGIDGHTLSDK 25

RESULT 3
QSVIL6 PRELIMINARY; PRT; 55 AA.
ID Q8VIL6
AC Q8VIL6;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Galanin-like peptide (Fragment).
GN Name=Galp;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=21569989; PubMed=11713207; DOI=10.1210/en.142.12.5140;
RA Jureus A., Cunningham M.J., Li D., Johnson L.L., Krasnow S.M.,
RA Tekemichael D.N., Clifton D.K., Steiner R.A.;
RT "Distribution and Regulation of Galanin-Like Peptide (GALP) in the
RT Hypothalamus of the Mouse.";
RL Endocrinology 142:5140-5144(2001).
DR EMBL; AF426450; AAL32205.1; -.
DR MGI; MGI:2663979; Galp.
DR GO; GO:0005102; P:receptor binding; TAS.
DR Pfam; PF01296; Galanin; 1.
DR PROSITE; PS00861; GALANIN; 1.
FT NON_TER 1 1
FT NON_TER 55 55
SQ SEQUENCE 55 AA; 5785 MW; 995DF6B2C7977D2 CRC64;

Query Match 51.9%; Score 69; DB 2; Length 115;
Best Local Similarity 85.7%; Pred. No. 0.038;
Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GWTLSAGYLLGKI 14
Db ||||| :
32 GWTLSAGYLLGPV 45

RESULT 5
GALP_HUMAN STANDARD; PRT; 116 AA.
ID GALP_HUMAN
AC Q9UBC7;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Galanin-like peptide precursor.
GN Name=GALP;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20069685; PubMed=10601261; DOI=10.1074/jbc.274.52.37041;
RA Ohtaki T., Kumano S., Ishibashi Y., Ogi K., Matsui H., Harada M.,
RA Kitada C., Kurokawa T., Onda H., Fujino M.;
RT "Isolation and cDNA cloning of a novel galanin-like peptide (GALP)
RT from porcine hypothalamus.";
RL J. Biol. Chem. 274:37041-37045(1999).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the galanin family.

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